

GenCore version 5.1.3
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OM protein - protein search, using sw model

Pub on January 16, 2003, 16:42:17 : Search time 24 seconds
(without alignments)
58,517 Million cell updates/sec

Title: US-09-856-070-17

Perfect score: 64
Sequence: 1 EREKQMMREKEEL 14

Scoring table: H09S062

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	69	100.0	581	2	145889	ezrin - bovine
2	69	100.0	586	1	A34400	ezrin [validated]
3	69	100.0	630	2	T47177	hypothetical prote
4	66	95.7	586	1	B41129	ezrin - mouse
5	51	73.9	577	1	A41289	moesin - human
6	51	73.9	577	1	S39804	moesin - pig
7	51	73.9	583	1	A46127	radixin - human
8	51	73.9	583	1	S39805	radixin - pig
9	51	73.9	583	1	A41129	radixin - mouse
10	51	73.9	451	2	T16634	hypothetical prote
11	47	68.1	1549	1	A40691	trichohyalin - she
12	45	65.2	365	2	T28184	hypothetical prote
13	44	63.8	166	2	T26620	hypothetical prote
14	44	63.8	406	2	T46674	hypothetical prote
15	44	63.8	555	2	T26657	unknown protein, 7
16	44	63.8	2962	2	T19756	hypothetical prote
17	43	62.3	86	2	H69809	hypothetical prote
18	43	62.3	229	2	T23700	conserved hypotet
19	43	62.3	233	2	T17218	hypothetical prote
20	43	62.3	547	2	T40314	hypothetical coile
21	43	62.3	743	2	A39232	18W malaria anti
22	43	62.3	813	2	T02672	hypothetical prote
23	43	62.3	1444	2	T42637	hypothetical prote
24	43	62.3	1407	1	S38589	trichohyalin - lab
25	43	62.3	1898	1	A45973	trichohyalin - hum
26	42	60.9	123	2	B81091	ribosome-binding f
27	42	60.9	123	2	B81851	ribosomal-binding
28	42	60.9	216	2	S64804	probable membrane
29	42	60.9	420	2	T47229	vitamin D receptor

30	42	60.9	453	2	T42438	mitochondrial proc
31	42	60.9	457	2	T50402	probable mitochond
32	42	60.9	471	1	S62590	peptidyl-prolyl ei
33	42	60.9	525	2	T48824	hypothetical prote
34	42	60.9	580	2	T40867	aspartate-tRNA lig
35	42	60.9	621	2	T51504	hypothetical prote
36	42	60.9	621	2	A57591	Id associated prot
37	42	60.9	849	1	S47432	scatfold attachmen
38	42	60.9	1156	2	B59444	chromosome segrega
39	42	60.9	1378	2	Q88637	protein P53H1.4 [i
40	42	60.9	4687	1	A39638	pectin - rat
41	41.5	60.1	220	2	H83967	hypothetical prote
42	41	59.4	85	1	IBWY	g-transferrin AI
43	41	59.4	94	2	S60794	M protein precurs
44	41	59.4	96	2	S60842	M protein precurs
45	41	59.4	235	2	T70405	hypothetical prote

ALIGNMENTS

RESULT 1

145889

ezrin - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 13-Aug-1999

C:Accession: 145889

R:Rerguson, C.M., Zhao, H., Salju, K., Duman, R.S., Nestler, E.J.

Mol. Cell. Neurosci. 4, 64-73, 1993

A:Title: Ezrin and osteonectin, two proteins associated with cell shape and growth, a

A:Reference number: 145889

A:Accession: 145889

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-581; SBER

A:Cross-references: GB M88498, MID 9289407, PIDN AAA30510.1, FID 9389408

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

F1:291/Domain: protein 4.1 membrane-binding domain homology <B41>

Query Match 100.0%, Score 69, DB 2, Length 581,

Best Local Similarity 100.0%, Pred. No. 0.031,

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

DB 334 EREKQMMREKEEL 347

RESULT 2

A34400

ezrin [validated] - human

N:Alternate names: cytoezrin, p81 protein; villin 2

C:Species: Homo sapiens (man)

C>Date: 30-Jul-1996 #sequence_revision 14-Jul-1994 #text_change 28-Feb-2000

C:Accession: A34400; S09263; E61002

E:Turunen, O.; Winiwiski, R.; Pakkanen, R.; Gieseler, K.H.; Wahlstrom, T.; Vaheri, A.

J. Biol. Chem. 264, 16727-16732, 1989

A:Title: Cytoezrin, a microvillar Mem 75,000 protein, cDNA sequence, prokaryotic exp

A:Reference number: A34400; MID:89380299, PMID:2574140

A:Accession: A34400

A:Molecule type: mRNA

A:Residues: 1-586; TUP

A:Cross-references: GB J05021

A:Note: the translation of residues 1-11 is not given

A:Note: parts of this sequence were confirmed by protein sequencing

E:Gould, K.L.; Friescher, A.; Esch, F.S.; Hunter, T.

EMBO J. 8, 4133-4142, 1989

A:Title: cDNA cloning and sequencing of the protein-tyrosine kinase substrate, ezrin,

A:Reference number: S09263; MID:90576135, PMID:2591371

A:Accession: S09263

A:Molecule type: mRNA

A:Residues: 2-586; TUP

A:Cross-references: GB X01201, MID 931582, PIDN AAA15873.1, FID 931583

R;Bauw, G.; Rasmussen, H.H.; Van den Buijck, M.; Van Lomme, J.; Feyffer, M.; Gesset, B.; O. Electrophoresis 11, 528-536, 1990
 A:Title: Two-dimensional gel electrophoresis, protein electrophoresis and microsequencing
 A:Reference number: A61002; PMID:91041404; PMID:1690755
 A:Accession: E61002
 A:Molecule type: protein
 A:Residues: 255-263;194, 195, 196, 199, 201, 264, 270, 285
 A:Note: it is not certain whether this material represents ezrin or radixin (see entry A61002)
 A:Note: This material corresponds to transformed epithelial amnion cell (AMA) database
 C:Comment: This protein is located in microvilli and is proposed to play a role in modulating cell motility
 C:Genetics:
 A:Gene: GDB:V112
 A:Cross-references: GDB:120489; OMIM:129300
 A:Map position: 6q25-6q26
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
 C:Keywords: actin binding; cytoskeleton; membrane associated protein, phosphoprotein
 F:2-586/Product: ezrin #status experimental <MAT>
 F:7-291/Domain: protein 4.1 membrane binding domain homology <B41>
 F:553-586/Region: actin binding #status predicted
 F:66/Binding site: phosphate (Ser) (covalent) #status predicted
 F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 69; DB 1; Length 586;
 Best Local Similarity 100.0%; Pred No. 0.042; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
 |||||
 DB 344 EREKQMMREKEEL 347

RESULT 3
 T47177
 hypothetical protein DKFZp762H157.1 human (fragment)
 C:Species: homo sapiens (man)
 C:Date: 20 Apr 2000 #sequence_revision 20 Apr 2000 #text_change 02-Sep-2000
 C:Accession: T47177
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24377
 A:Accession: T47177
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-630 <AAA>
 A:Cross-references: EMBL:AL162086
 A:Experimental source: adult melanoma (MeWo cell line); clone DKFZp762H157
 C:Genetics:
 A:Note: DKFZp762H157.1
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

Query Match 100.0%; Score 69; DB 2; Length 630;
 Best Local Similarity 100.0%; Pred No. 0.042; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
 |||||
 DB 378 EREKQMMREKEEL 391

RESULT 4
 H41129
 ezrin - mouse
 N:Alternate names: cytovillin; p81 protein; radixin; villin 2
 C:Species: Mus musculus (house mouse)
 C:Date: 03 Aug 1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
 C:Accession: H41129; C46501; A46501; B46501; S24203
 R:Funayama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.
 J. Cell Biol. 115, 1039-1048, 1991
 A:Title: Radixin is a novel member of the band 4.1 family.
 A:Reference number: A41129; PMID:92064645; PMID:1955455
 A:Accession: B41129
 A:Molecule type: mRNA
 A:Residues: 1-586 <FUN>

A:Cross-references: EMBL:X00671; NID:950880; PIDD:CA443086.1; PIDD:q50881
 R:Eschberg, M.; Burgess, W.H.; Chen, B.; Drucker, B.J.; Bretscher, A.; Samelson, L.E. J. Immunol. 149, 1847-1852, 1992
 A:Title: Identification of ezrin as an 81 kDa tyrosine phosphorylated protein in T cell
 A:Reference number: A46501; PMID:92388649; PMID:1381389
 A:Accession: C46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 412-425 <EGE>
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112938)
 A:Accession: A46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-33; 'E' <E32>
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112936)
 A:Accession: B46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 53-57;148, 'L',150, 'G',152-155 <EG3>
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112940)
 C:Comment: This protein is located in microvilli and is proposed to play a role in morphogenesis
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
 C:Keywords: actin binding; cytoskeleton; cytosol; membrane-associated protein; phosphoprotein
 F:2-586/Product: ezrin #status predicted; <MAT>
 F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:553-586/Region: actin binding #status predicted
 F:66/Binding site: phosphate (Ser) (covalent) #status predicted
 F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 95.7%; Score 66; DB 1; Length 586;
 Best Local Similarity 92.4%; Pred No. 0.081; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
 |||||
 DB 334 EREKQMMREKEEL 347

RESULT 5
 moesin - human
 N:Alternate names: membrane-organizing extension spike protein
 C:Species: homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A41289
 R:Jankes, W.T.; Farthmayr, H.; Pross, N.; Acad. Sci. U.S.A. 88, 8297-8301, 1991
 A:Title: Moesin, a member of the protein 4.1-talin-ezrin family of proteins.
 A:Reference number: A41289; PMID:92030840; PMID:1924289
 A:Accession: A41289
 A:Molecule type: mRNA
 A:Residues: 1-577 <LAN>
 A:Cross-references: GDB:M69096; NID:glb8925; PIDD:AAA36322.1; PIDD:glb8926
 C:Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasma membrane
 C:Genetics:
 A:Gene: GDB:MSN
 A:Cross-references: GDB:136819; OMIM:309845
 A:Map position: Xq11.2-Xq12
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
 C:Keywords: actin binding; cytoskeleton; membrane protein
 F:2-577/Product: moesin #status predicted <MAT>
 F:7-291/Domain: protein 4.1 membrane binding domain homology <B41>
 F:544-577/Region: actin binding #status predicted

Query Match 73.9%; Score 51; DB 1; Length 577;
 Best Local Similarity 71.4%; Pred. No. 9.1; Mismatches 3; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
 |||||

Db 334 EKEKIEPEKEEL 347

RESULT 6

moesin - pig

N:Alternate names: membrane-organizing extension spike protein

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999

C:Accession: S39804

R:Links: W.T.: Schwartz-Albiez, R.; Furthmayr, H.

Biochim. Biophys. Acta 1216, 479-482, 1993

A:Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification of

F:7-291/Domain: protein 4.1 membrane-binding domain homology

A:Reference number: S39804, MUID:94092743, PMID:8268231

A:Accession: S39804

A:Molecule type: mRNA

A:Residues: 1-577

A:Cross-references: EMBL:M86344; F100:q14545; F100:q14546; F100:q14547; F100:q14548

C:Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasma

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton; membrane protein

F:2-577/Product: moesin #status predicted <MAT>

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:544-577/Region: actin binding #status predicted

Query Match 73.9% Score 51; DB 1; Length 577;

Best Local Similarity 71.4%; Pred No. 9.1;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

Db 334 EKEKIEPEKEEL 347

RESULT 7

A46127

radixin - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1993 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999

C:Accession: A46127

R:Wilgenbus, K.K.; Milatovich, A.; Francke, U.; Furthmayr, H.

Genomics 16, 199-206, 1993

A:Title: Multicatalytic cDNA sequence, and subcellular distribution of the human radixin

A:Reference number: A46127; MUID:94092478; PMID:8486157

A:Accession: A46127

A:Molecule type: mRNA

A:Residues: 1-583

A:Cross-references: GR:102320; NID:q307365; PID:q307366

A:Note: sequence extracted from NCBI backbone (NCBIN_131481, NCBIPI_131482)

C:Comment: Radixin is a capping protein for the barbed ends of actin filaments and it is

C:Genetics:

A:Gene: GDB:RDX

A:Cross-references: GR:136270; OMIM:179410

A:Map position: 11q23-11q23

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:470-477/Region: proline-rich

F:550-583/Region: actin binding #status predicted

Query Match 73.9% Score 51; DB 1; Length 583;

Best Local Similarity 71.4%; Pred No. 9.2;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

Db 334 EKEKIEPEKEEL 347

RESULT 8

S39805

radixin - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999

C:Accession: S39805

R:Links: W.T.: Schwartz-Albiez, R.; Furthmayr, H.

Biochim. Biophys. Acta 1216, 479-482, 1993

A:Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification

F:7-291/Domain: protein 4.1 membrane-binding domain homology

A:Reference number: S39804, MUID:94092743, PMID:8268231

A:Accession: S39805

A:Molecule type: mRNA

A:Residues: 1-583

A:Cross-references: GR:M86344; F100:q14545; F100:q14546; F100:q14547; F100:q14548

C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:470-477/Region: proline-rich

F:550-583/Region: actin binding #status predicted

Query Match 73.9% Score 51; DB 1; Length 583;

Best Local Similarity 71.4%; Pred No. 9.2;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

Db 334 EKEKIEPEKEEL 347

RESULT 9

A41129

radixin - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Aug-1992 #sequence_revision 14-Jul-1994 #text_change 05-Sep-1997

C:Accession: A41129; S24201

R:Furuyama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.

J. Cell Biol. 115, 1039-1048, 1991

A:Title: Radixin is a novel member of the band 4.1 family.

A:Reference number: A41129; MUID:92064635; PMID:1955455

A:Accession: A41129

A:Molecule type: mRNA

A:Residues: 1-63; FUN.

A:Cross-references: EMBL:X69672; NID:q1033049; PID:q1334260

A:Note: part of this sequence was confirmed by protein sequencing

C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:470-477/Region: proline-rich

F:550-583/Region: actin binding #status predicted

Query Match 73.9% Score 51; DB 1; Length 583;

Best Local Similarity 71.4%; Pred No. 9.2;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

Db 334 EKEKIEPEKEEL 347

RESULT 10

T15624

hypothetical protein C25H3.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: T15624

R:Johnson, D.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid C25H3.

A:Reference number: Z18379

A:Accession: T15624

A>Status: preliminary; translated from GR/EMBL/DDHU

A:Molecule type: DNA

A:Residues: 1-651 <JOH>

A:Cross-references: EMBL:M86344; NID:q14545; F100:q14546; F100:q14547; F100:q14548

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:C25H3.6
A:Introns: 58/1, 213/3, 273/3 139 2, 478/2 184/2, 510/2 552/3, 677/2

Query Match

Best Local Similarity 73.9% Score 51; DB 2; Length 651;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKE 12

|||||:|||||

DB 335 EREKQMMREKE 346

RESULT 11

A40691

Trichohyalin - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 21 Sep 1993 #sequence_revision 6; 31 Mar 1996 #text_change 22-Jun 1999

C:Accession: A40691; A34209; S32633

R:Fieldz, M.J.; McCaughlan, C.J.; Campbell, M.T.; Rogers, G.E.

J. Cell Biol. 121, 855-865, 1993

A:Title: Analysis of the sheep trichohyalin gene: potential structural and calcium-binding

A:Reference number: A40691; MUID:93260018; PMID:7684041

A:Accession: A40691

A:Molecule type: DNA

A:Residues: 1-1549 <IE>

A:Cross-references: EMBL:Z18361; NID:q295940; PIDN:CAA79165 1; PID:q295941

A:Note: Sequence extracted from NCHI backbone (NCHIP:132511)

R:Fieldz, M.J.; Presland, R.H.; Rogers, G.E.

J. Cell Biol. 110, 427-436, 1990

A:Title: The cDNA-deduced amino acid sequence for trichohyalin, a differentiation marker

A:Reference number: A34209; MUID:90130532; PMID:2298812

A:Accession: A34209

A:Molecule type: mRNA

A:Residues: 1016-1151, 1205-1257, 1291-1306, 1377-1400 1549 <F2>

A:Cross-references: GB:X51695; NID:q1827; PIDN:CAA35992 1; PID:q1828

C:Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root sheath

covalent modifications to this protein include conversion of arginine to citrulline and

C:Genetics:

A:Introns: 46/3

A:Note: single copy gene

C:Superfamily: trichohyalin; calmodulin repeat homology

C:Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat

F:49-81/Domain: calmodulin repeat homology <EF>

F:187-851/Region: 28-residue repeats

F:1886-1519/Region: 23 residue repeats

Query Match

Best Local Similarity 68.1% Score 47; DB 1; Length 1549;

Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 EREKQMMREKEEL 14

|||||:|||||

DB 1172 EREKQMMREKEEL 1184

RESULT 12

T28184

hypothetical protein ORF23 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon)

N:Alternate names: ORF MSV023 AL1 motif gene family protein

C:Species: Melanoplus sanguinipes entomopoxvirus

A:Variety: isolate Tuscon

C:Date: 21-Jan-2000 #sequence_revision 21-Jan 2000 #text_change 21-Jul 2000

C:Accession: T28184

R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, C.F.; Rock, D.L.

J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: 220484; MUID:q9102612; PMID:9447359

A:Accession: T28184

A:Status: preliminary; translated from GH/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-365 <AF0>

A:Cross-references: EMBL:AF063866; NID:q4049647; PIDN:AA097848 1; PID:q4049888

A:Experimental source: isolate Tuscon

C:Genetics:

A:Note: MSV023

Query Match

Best Local Similarity 65.2% Score 45; DB 2; Length 465;

Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EREKQMMREKEEL 14

|||||:|||||

DB 114 EREKQMMREKEEL 126

RESULT 13

I39620

hypothetical protein SPBCL6H5.15 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03 Nov 1999 #sequence_revision 03 Dec 1999 #text_change 03-Dec-1999

C:Accession: I39620

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skellton, J.; Chutcher, C.M.

submitted to the EMBL Data Library, March 1998

A:Reference number: Z21843

A:Accession: I39620

A:Status: preliminary; translated from GR/EMBL/DDDBJ

A:Molecule type: DNA

A:Residues: 1-165 <W0>

A:Cross-references: EMBL:AL022104; PIDN:CAH60139 1; GSPDB:GN03067, SPDB:SPBCL6H5.15

A:Experimental source: strain 972h-; cosmid c16H5

C:Genetics:

A:Gene: SPDB:SPBCL6H5.15

A:Map position: 2

Query Match

Best Local Similarity 63.8% Score 44; DB 2; Length 166;

Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKE 12

|||||:|||||

DB 80 KKEKQMLKEKE 91

RESULT 14

F96679

hypothetical protein F5114.2 [imported] Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar 2001 #sequence_revision 02 Mar 2001 #text_change 31-Mar 2001

C:Accession: F96679

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Cona, L.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizlar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Ma, K.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: F96679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-406 <STO>

A:Cross-references: GR:Ar05173; NID:q2190549; PIDN:AA950931 1; GSPDB:GH00141

C:Genetics:

A:Gene: F5114.2

A:Map position: 1

Query Match

Best Local Similarity 63.8% Score 44; DB 2; Length 406;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EREKQMMREKEE 13

|||||:|||||

Db 311 ESEKQKREKEEL 323

RESULT 15

C96667

unknown protein, 71502-69704 [imported] - Arabidopsis thaliana

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C:Date: 02 Mar 2001 #sequence_revision 02 Mar 2001 #text_change 31 Mar 2001

C:Accession: C96667

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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

anssen, N.F.; Hughes, B.; Huizar, L.

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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

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A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: C96667

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-555 <SI>

A:Cross-references: GR AK005173, NID:gl0645451, F10N.AA321515.1; GSPDR:GN00141

C:Genetics:

A:Gene: F15H21.4

A:Map position: 1

Query Match

Best Local Similarity 63.8%; Score 44; DB 2; Length 555;

Matches 7; Conservative 6; Mismatches 1; Indels 0; Caps 0;

QY 1 EREKQMMREKEEL 14

DB 473 ANFKDPMAREKEEV 486

Search completed: January 16, 2003, 16:57:47
Job time : 24 secs

